WHAT IS CLAIMED IS:

1. A method for analyzing exon expression in a cell sample, comprising measuring the expression levels of a plurality of individual exons or multiexons in each of a plurality of different genes in the genome of an organism from which said cell sample is derived, wherein the measured expression level of each exon or multiexon is not averaged with the measured expression level of one or more different exons or multiexons in the same gene; thereby analyzing the exon expression of said cell sample.

2. The method of claim 1, wherein said measured expression levels are used to determine a distinguishing structural characteristic of an expressed variant for each of one or more of said exons or multiexons.

3. The method of claim 2, wherein the structural characteristic of said expressed variant for each of one or more of said exons or multiexons is determined by determining the length of said expressed variant.

4. The method of claim 1, wherein said plurality of individual exons or multiexons consists of at least 3 different exons or multiexons.

5. The method of claim 1, wherein said plurality of individual exons or multiexons consists of at least 5 different exons or multiexons.

6. The method of claim 1, wherein said plurality of individual exons or multiexons consists of at least two different exons.

7. The method of claim 1, 4, 5 or 6, wherein said plurality of different genes consists of at least 100 different genes.

8. The method of claim 1, 4, 5 or 6, wherein said plurality of different genes consists of at least 1,000 different genes.

9. The method of claim 1, 4, 5 or 6, wherein said plurality of different genes consists of at least 10,000 different genes.

10. The method of claim 1, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a

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sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon of said cell sample; and

(b) measuring hybridization between said probes and said RNAs or nucleic acids.

11. The method of claim 10, wherein said plurality of individual exons or multiexons consists of at least 3 different exons.

12. The method of claim 10, wherein said plurality of individual exons or multiexons consists of at least 5 different exons.

13. The method of claim 10, 11 or 12, wherein said plurality of different genes consists of at least 1,000 different genes.

14. The method of claim 10, wherein said plurality of polynucleotide probes consists of at least 100 different polynucleotide probes.

15. The method of claim 10, wherein said plurality of polynucleotide probes consists of at least 1,000 different polynucleotide probes.

16. The method of claim 10, wherein said plurality of polynucleotide probes consists of at least 10,000 different polynucleotide probes.

17. The method of claim 10, wherein said plurality of polynucleotide probes is in the range of 1,000 to 50,000 different polynucleotide probes.

18. The method of claim 10, wherein said positionally-addressable array has in the range of 100 to 1,000 different polynucleotide probes per 1 cm^2.

19. The method of claim 10, wherein said positionally-addressable array has in the range of 1,000 to 10,000 different polynucleotide probes per 1 cm^2.

20. The method of claim 10, wherein said positionally-addressable array has in the range of 10,000 to 50,000 different polynucleotide probes per 1 cm^2.

21. The method of claim 10, wherein said positionally-addressable array has more than 50,000 different polynucleotide probes per 1 cm^2.

22. The method of claim 10, wherein each of said different nucleotide sequences consists of 10 to 1,000 nucleotides.

23. The method of claim 10, wherein each of said different nucleotide sequences consists of 15 to 600 nucleotides.

24. The method of claim 10, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

25. The method of claim 10, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

26. The method of claim 10, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

27. The method of claim 10, wherein each of said different nucleotide sequences consists of 60 nucleotides.

28. The method of claim 10, wherein at least one probe in said plurality of probes contains, in addition to said sequence complementary and hybridizable to a different exon or multiexon, linker sequences.

29. The method of claim 28, wherein said linker sequence comprises a linker sequence between said sequence complementary and hybridizable to a different exon or multiexon and said support.

30. The method of claim 10, wherein said sequence is complementary to the sequence of a full length exon.

31. The method of claim 10, wherein at least one of said plurality of polynucleotide probes

comprises a nucleotide sequence complementary and hybridizable to a multiexon.

32. The method of claim 31, wherein the nucleotide sequence of said at least one polynucleotide probe is complementary to a sequence spanning the splice junction between different exons in said multiexon.

33. The method of claim 31, wherein said sequence is complementary to a sequence comprising a full length exon flanked by sequences from adjacent exon or exons in said multiexon.

34. The method of claim 10, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

35. The method of claim 1 or 10, wherein said expression levels are measured as continuous variables.

36. The method of claim 35, wherein said expression levels are measured as continuous variables and represented as absolute abundance.

37. A method for analyzing exon expression of a cell sample, comprising measuring the expression levels of all individual exons or multiexons in each of a plurality of different genes in the genome of an organism from which said cell sample is derived, thereby analyzing the exon expression of said cell sample.

38. A method for determining the presence or absence of alternatively spliced mRNAs for a plurality of genes in a cell sample, comprising

(a) measuring the expression levels of a plurality of individual exons or multiexons in each of a plurality of different genes in the genome of an organism from which said cell sample is derived, wherein said plurality of exons is sufficient to distinguish a plurality of alternative splicing pathways; and

(b) determining the presence or absence of alternatively spliced mRNAs in said sample based on said measured expression levels.

39. The method of claim 37 or 38, wherein said plurality of different genes is 5 to 10

different genes.

40. The method of claim 37 or 38, wherein said plurality of different genes is 10 to 100 different genes.

41. The method of claim 37 or 38, wherein said plurality of different genes is 100 to 1,000 different genes.

42. The method of claim 37 or 38, wherein said plurality of different genes is 1,000 to 10,000 different genes.

43. The method of claim 37 or 38, wherein said plurality of different genes is more than 10,000 different genes.

44. The method of claims 37 or 38, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon of said cell sample; and

(b) measuring hybridization between said probes and said RNAs or nucleic acids.

45. The method of claim 1, 10, 37, or 38, wherein said organism is a human.

46. The method of claim 1, 10, 37, or 38, wherein said organism is a plant.

47. A method for determining the exon expression state of a cell sample, comprising:

(a) measuring the expression levels of a plurality of individual exons or multiexons in each of a plurality of different genes in the genome of an organism from which said cell sample is derived; and

(b) representing the exon expression state of said cell sample as a collection of

individual values of said measured expression level for each exon or multiexon in said plurality of individual exons or multiexons; thereby determining the exon expression state of said cell sample.

48. A method for determining the exon expression state of a chromosome of an organism in a cell sample, comprising:

(a) measuring the expression levels of a plurality of individual exons or multiexons in each of a plurality of different genes in said chromosome; and

(b) representing the exon expression state of said chromosome as a collection of individual values of said measured expression level for each exon or multiexon in said plurality of individual exons or multiexons; thereby determining the exon expression state of said chromosome of said cell sample.

49. The method of claim 48, wherein said chromosome is human chromosome 22.

50. The method of claim 47, wherein said plurality of individual exons or multiexons consists of at least 3 different exons or multiexons.

51. The method of claim 47, wherein said plurality of individual exons or multiexons consists of at least 5 different exons or multiexons.

52. The method of claim 47, wherein said plurality of individual exons or multiexons consists of at least two different exons.

53. The method of claim 47, 50, 51 or 52, wherein said plurality of different genes consists of at least 100 different genes.

54. The method of claim 47, 50, 51 or 52, wherein said plurality of different genes consists of at least 1,000 different genes.

55. The method of claim 47, 50, 51 or 52, wherein said plurality of different genes consists of at least 10,000 different genes.

56. The method of claim 47, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a

sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon of said cell sample; and

(b) measuring hybridization between said probes and said RNAs or nucleic acids.

57. The method of claim 56, wherein said plurality of individual exons or multiexons consists of at least 3 different exons.

58. The method of claim 56, wherein said plurality of individual exons or multiexons consists of at least 5 different exons.

59. The method of claim 56, 57 or 58, wherein said plurality of different genes consists of at least 1,000 different genes.

60. The method of claim 56, wherein said plurality of polynucleotide probes consists of at least 100 different polynucleotide probes.

61. The method of claim 56, wherein said plurality of polynucleotide probes consists of at least 1,000 different polynucleotide probes.

62. The method of claim 56, wherein said plurality of polynucleotide probes consists of at least 10,000 different polynucleotide probes.

63. The method of claim 56, wherein said plurality of polynucleotide probes is in the range of 1,000 to 50,000 different polynucleotide probes.

64. The method of claim 56, wherein said positionally-addressable array has in the range of 100 to 1,000 different polynucleotide probes per 1 cm^2.

65. The method of claim 56, wherein said positionally-addressable array has in the range of 1,000 to 10,000 different polynucleotide probes per 1 cm^2.

66. The method of claim 56, wherein said positionally-addressable array has in the range of 10,000 to 50,000 different polynucleotide probes per 1 cm^2.

67. The method of claim 56, wherein said positionally-addressable array has more than 50,000 different polynucleotide probes per 1 cm^2.

68. The method of claim 56, wherein each of said different nucleotide sequences consists of 10 to 1,000 nucleotides.

69. The method of claim 56, wherein each of said different nucleotide sequences consists of 15 to 600 nucleotides.

70. The method of claim 56, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

71. The method of claim 56, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

72. The method of claim 56, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

73. The method of claim 56, wherein each of said different nucleotide sequences consists of 60 nucleotides.

74. The method of claim 56, wherein at least one probe in said plurality of probes contains, in addition to said sequence complementary and hybridizable to a different exon or multiexon, linker sequences.

75. The method of claim 74, wherein said leading sequence comprises a spacer sequence between said sequence complementary and hybridizable to a different exon or multiexon and said support.

76. The method of any of claim 56, wherein said sequence is complementary to the sequence of a full length exon.

77. The method of any of claim 56, wherein at least one of said plurality of polynucleotide

probes comprises a nucleotide sequence complementary and hybridizable to a multiexon.

78. The method of claim 77, wherein the nucleotide sequence of said at least one polynucleotide probe is complementary to a sequence spanning the splice junction between different exons in said multiexon.

79. The method of claim 77, wherein said sequence is complementary to a sequence comprising a full length exon flanked by sequences from adjacent exon or exons in said multiexon.

80. The method of claim 56, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

81. The method of claim 47 or 56, wherein said expression levels are measured as continuous variables.

82. The method of claim 81, wherein said expression levels are measured as continuous variables and represented as absolute abundance.

83. A method for determining the exon expression state of a cell sample, comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism from which said cell sample is derived, wherein said different exons or multiexons comprise a plurality of individual exons or multiexons of each of a plurality of different genes in the genome of said organism, and wherein said array does not comprise a second plurality of polynucleotide probes that do not comprise a sequence complementary and hybridizable to said genome of said organism, said second plurality being of equal or greater number than said first plurality; and

(b) measuring hybridization between said probes and said RNAs or nucleic acids.

84. A method for determining the exon expression state of a cell sample, comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence designed to be complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism from which said cell sample is derived, wherein said different exons or multiexons comprise a plurality of exons or multiexons in each of a plurality of different genes in the genome of said organism; and

(b) measuring hybridization between said probes and said RNAs or nucleic acids.

85. The method of claim 47, further comprising determining the exon content of different mRNA transcripts of each of the plurality of genes based on said measured expression levels; thereby determining the transcriptional state of said cell sample.

86. The method of claim 1, 10, 47 or 83, wherein said cell sample has been subjected to a perturbation.

87. The method of claim 86, wherein said organism is a human.

88. The method of claim 86, wherein said organism is a plant.

89. The method of claim 86, further comprising comparing the expression levels of at least a portion of said plurality of individual exons or multiexons in said cell sample having been subjected to said perturbation with the expression level of said portion of said plurality of individual exons or multiexons in a cell sample of the same type not having been subjected to said perturbation.

90. The method of claim 89, wherein said comparing comprises determining the difference

between the expression level of each exon or multiexon in said portion of said plurality of individual exons or multiexons in said cell sample having been subjected to said perturbation and the expression level of the corresponding exons or multiexons in said cell sample of the same type not having been subjected to said perturbation.

91. An array comprising a positionally-addressable array of polynucleotide probes bound to a support, said polynucleotide probes comprising a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of said support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism, wherein said different exons or multiexons comprise a plurality of individual exons or multiexons of each of a plurality of different genes in the genome of said organism, and wherein said polynucleotide probes comprise junction specific probes.

92. The array of claim 91 wherein said plurality of polynucleotide probes are bound to said support covalently at the 3' or 5' end of each polynucleotide probe.

93. An array comprising a positionally-addressable array of polynucleotide probes bound to a support, said polynucleotide probes comprising a plurality of polynucleotide probes of different nucleotide sequences, each of said different nucleotide sequences comprising a sequence designed to be complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism, wherein said different exons or multiexons comprise a plurality of individual exons or multiexons of each of a plurality of different genes in the genome of said organism.

94. The array of claim 93 wherein said plurality of polynucleotide probes are bound to said support covalently at the 3' or 5' end of each polynucleotide probe.

95. An array comprising a positionally-addressable array of polynucleotide probes bound to a support, said polynucleotide probes comprising a plurality of polynucleotide probes of different nucleotide sequences, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon in a plurality of genes in the genome of an organism, wherein said different exons or multiexons comprise a plurality of individual exons or multiexons of each of a plurality of different genes in the genome of said organism, wherein the plurality of different exons or multiexons for each of said different genes comprises a set of exons that is sufficient to

distinguish a plurality of alternative splicing pathways.

96. The array of claim 95 wherein said plurality of polynucleotide probes are bound to said support covalently at the 3' or 5' end of each polynucleotide probe.

97. The array of any of claims 91-96, said polynucleotide probes comprising a set of successive overlapping probes spanning the longest known or predicted variant of an exon.

98. The array of any of claims 91-96, said polynucleotide probes comprising a set of junction specific probes, each said junction specific probe being specifically hybridizable to a different junction region in a different variant of said exon.

99. The array of claim 98, said polynucleotide probes further comprising exon specific probes specifically hybridizable to common sequences among a plurality of variants of an exon.

100. The array of claim 91, wherein said different exons or multiexons consists of at least 3 different exons or multiexons.

101. The array of claim 91, wherein said different exons or multiexons consists of at least 5 different exons or multiexons.

102. The array of any of claim 91, wherein said different exons or multiexons consists of at least 2 different exons.

103. The array of any of claims 91-96 and 100-102, wherein said plurality of different genes consists of at least 100 genes.

104. The array of any of claims 91-96 and 100-102, wherein said plurality of different genes consists of 100 to 1,000 genes.

105. The array of any of claims 91-96 and 100-102, wherein said plurality of different genes consists of 1,000 to 10,000 genes.

106. The array of any of claims 91-96 and 100-102, wherein said plurality of different genes consists of 10,000 to 50,000 genes.

107. The array of any of claims 91-96 and 100-102, wherein said plurality of different genes consists of more than 50,000 genes.

108. The array of any of claims 91-96, wherein said positionally-addressable array has in the range of 100 to 1,000 different polynucleotide probes per 1 cm^2.

109. The array of any of claims 91-96, wherein said positionally-addressable array has in the range of 1,000 to 10,000 different polynucleotide probes per 1 cm^2.

110. The array of any of claims 91-96, wherein said positionally-addressable array has in the range of 10,000 to 50,000 different polynucleotide probes per 1 cm^2.

111. The array of any of claims 91-96, wherein said positionally-addressable array has more than 50,000 different polynucleotide probes per 1 cm^2.

112. The array of any of claims 91-96, wherein each of said different nucleotide sequences consists of 10 to 1,000 nucleotides.

113. The array of any of claims 91-96, wherein each of said different nucleotide sequences consists of 15 to 600 nucleotides.

114. The array of any of claims 91-96, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

115. The array of any of claims 91-96, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

116. The array of any of claims 91-96, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

117. The array of any of claims 91-96, wherein each of said different nucleotide sequences consists of 60 nucleotides.

118. The array of any of claims 91-96, wherein at least one probe in said plurality of probes contains, in addition to said sequence complementary and hybridizable to a different exon or multiexon, linker sequences.

119. The array of claim 118, wherein said leading sequence comprises a spacer sequence between said sequence complementary and hybridizable to a different exon or multiexon and said support.

120. The array of any of claims 91-96, wherein said sequence is complementary to the sequence of a full length exon.

121. The array of any of claims 91-96, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a multiexon.

122. The array of claim 121, wherein the nucleotide sequence of said at least one polynucleotide probe is complementary to a sequence spanning the splice junction between different exons in said multiexon.

123. The array of claim 121, wherein said sequence is complementary to a sequence comprising a full length exon flanked by sequences from adjacent exon or exons in said multiexon.

124. The array of any of claims 91-96, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

125. The array of any of claims 91-96, further comprising a sample comprising a population of cellular RNA or nucleic acids derived therefrom on the surface of said support such that said sample is in contact with said polynucleotide probes, under conditions conducive to hybridization between said population and said polynucleotide probe.

126. The array of claim 125, wherein said population is labeled.

127. The array of claim 125, wherein said population comprises nucleic acids of at least 10,000 different sequences.

128. An array comprising a positionally-addressable array of polynucleotide probes bound to a support, said polynucleotide probes comprising a plurality of polynucleotide probes of different nucleotide sequences, each of said different nucleotide sequences comprising a

sequence designed to be complementary and hybridizable to a sequence spanning the junction region of a multiexon in the genome of an organism.

129. A set of positionally-addressable arrays of polynucleotide probes, said set in total comprising for each of all known or predicted exons or multiexons in the genome of an organism at least one polynucleotide probe comprising a sequence complementary and hybridizable to a sequence in only one of said exons or multiexons.

130. The set of arrays of claim 129, comprising for each of said known or predicted exon in the genome of said organism two polynucleotide probes each comprising a different sequence complementary and hybridizable to a sequence in only one of said exons or multiexons.

131. The set of arrays of claim 129 or 130, wherein said organism is human.

132. The set of arrays of claim 129 or 130, wherein said organism is a plant.

133. The set of arrays of claim 129 or 130, wherein said organism is a fungus.

134. A method for preparing an array of polynucleotide probes comprising synthesizing a plurality of polynucleotide probes of different nucleotide sequences on a support, wherein

polynucleotide probes of different sequence are synthesized at different regions on said support so as to form a positionally-addressable array;

each of said plurality of polynucleotide probes comprises a sequence complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism, wherein said different exons or multiexons comprise a plurality of individual exons or multiexons of each of a plurality of different genes in the genome of said organism; and

said array does not comprise a second plurality of polynucleotide probes that do not comprise a sequence complementary and hybridizable to said genome of said organism, said second plurality being of equal or greater number than said first plurality.

135. A method for preparing an array of polynucleotide probes comprising depositing a plurality of polynucleotide probes on a support, wherein

polynucleotide probes of different sequence are deposited at different regions on said support so as to form a positionally-addressable array;

each of said plurality of polynucleotide probes comprises a sequence complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism, wherein said different exons or multiexons comprise a plurality of individual exons or multiexons of each of a plurality of different genes in the genome of said organism; and

said array does not comprise a second plurality of polynucleotide probes that do not comprise a sequence complementary and hybridizable to said genome of said organism, said second plurality being of equal or greater number than said first plurality.

136. A method for preparing an array of polynucleotide probes comprising synthesizing a plurality of polynucleotide probes of different nucleotide sequence on a support, wherein

polynucleotide sequences of different sequences are synthesized at different regions on said support so as to form a positionally-addressable array; and

each of said plurality of probes comprises a sequence designed to be complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism, wherein said different exons or multiexons comprise a plurality of individual exons or multiexons of each of a plurality of different genes in the genome of said organism.

137. A method for preparing an array of polynucleotide probes comprising depositing a plurality of polynucleotide probes of different nucleotide sequences on a support, wherein

polynucleotide probes of different sequence are deposited at different regions on said support so as to form a positionally addressable array; and

each of said plurality of probes comprises a sequence designed to be complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism, wherein said different exons or multiexons comprise a plurality of individual exons or multiexons of each of a plurality of different genes in the genome of said organism.

138. A method for determining the relative level of expression of individual exons in a gene, for a plurality of different genes, in a cell sample, comprising

(a) measuring for a plurality of genes in said cell sample the expression level of at least a first exon and a second exon in the same gene; and

(b) comparing said measured expression level of said first exon to the expression level of said second exon or the measured expression levels of more than one exon in said same gene, for each of said plurality of genes.

139. The method of claim 138, wherein said plurality of different genes consists of at least 100 different genes.

140. The method of claim 138, wherein said plurality of different genes consists of at least 1,000 different genes.

141. The method of claim 138, wherein said plurality of different genes consists of at least 10,000 different genes.

142. The method of claim 138, wherein in step (a), the expression levels of at least 3 exons in said same gene are measured.

143. The method any one of claims 138-142, further comprising expressing said measured expression level as a ratio of said measured expression level of said first exon to the measured expression level of said second exon or the measured expression levels of more than one exon in said same gene.

144. The method of any one of claims 138-142, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon of said cell sample; and

(b) measuring hybridization between said probes and said RNAs or nucleic acids.

145. The method of claim 144, further comprising expressing said measured expression level as a ratio of said measured expression level of said first exon to the measured expression level of said second exon or the measured expression levels of more than one exon in said same gene.

146. A method for detecting alternative splicing between two cell samples of a species of an

organism, comprising

(a) measuring in a first cell sample of said species the expression levels of a plurality of individual exons or multiexons in each of a plurality of different genes;

(b) measuring in a second cell sample of said species the expression levels of said plurality of individual exons or multiexons in each of said plurality of different genes; and

(c) comparing the measured expression level of each exon or multiexon in said first cell sample to the measured expression level of the same exon or multiexon in said second cell sample to identify differences in the expression levels of one or more exons or multiexons, wherein said identified differences indicates alternative splicings between said first and second cell samples.

147. The method of claim 146, wherein said plurality of individual exons or multiexons in each of said plurality of different genes consists of at least 3 different exons or multiexons.

148. The method of claim 146, wherein said plurality of individual exons or multiexons in each of said plurality of different genes consists of at least 5 different exons or multiexons.

149. The method of claim 146, wherein said plurality of individual exons or multiexons in each of said plurality of different genes consists of a plurality of individual exons.

150. The method of claim 146, wherein said plurality of individual exons or multiexons in each of said plurality of different genes comprises all exons in each gene.

151. A method for analyzing the transcriptional state of a cell sample, comprising measuring the expression level of each of a plurality of different mRNAs expressed by said cell sample; and determining the exon content of said different mRNAs based on said measured expression levels.

152. The method of claim 151, wherein said plurality of different mRNAs consists of more than 10 different mRNA transcripts.

153. The method of claim 151, wherein said plurality of different mRNAs consists of more than 100 different mRNA transcripts.

154. The method of claim 151, wherein said plurality of different mRNAs consists of more than 1,000 different mRNA transcripts.

155. The method of claim 151, wherein said plurality of different mRNAs consists of at least 10,000 different mRNAs.

156. The method of claim 151, wherein said plurality of different mRNAs consists of at least 50,000 different mRNAs.

157. The method of claim 1, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a sequence in a different exon or multiexon in the genome of an organism from which said cell sample is derived; and

(b) measuring hybridization between said probes and said RNAs or nucleic acids.

158. The method of claim 157, wherein said plurality of individual exons or multiexons consists of at least 3 different exons.

159. The method of claim 157, wherein said plurality of individual exons or multiexons consists of at least 5 different exons.

160. The method of claim 157, 158 or 159, wherein said plurality of different genes consists of at least 1,000 different genes.

161. The method of claim 157, wherein said plurality of polynucleotide probes consists of at least 100 different polynucleotide probes.

162. The method of claim 157, wherein said plurality of polynucleotide probes consists of at least 1,000 different polynucleotide probes.

163. The method of claim 157, wherein said plurality of polynucleotide probes consists of at least 10,000 different polynucleotide probes.

164. The method of claim 157, wherein said plurality of polynucleotide probes is in the range of 1,000 to 50,000 different polynucleotide probes.

165. The method of claim 157, wherein said positionally-addressable array has in the range of 100 to 1,000 different polynucleotide probes per 1 cm^2.

166. The method of claim 157, wherein said positionally-addressable array has in the range of 1,000 to 10,000 different polynucleotide probes per 1 cm^2.

167. The method of claim 157, wherein said positionally-addressable array has in the range of 10,000 to 50,000 different polynucleotide probes per 1 cm^2.

168. The method of claim 157, wherein said positionally-addressable array has more than 50,000 different polynucleotide probes per 1 cm^2.

169. The method of claim 157, wherein each of said different nucleotide sequences consists of 10 to 1,000 nucleotides.

170. The method of claim 157, wherein each of said different nucleotide sequences consists of 15 to 600 nucleotides.

171. The method of claim 157, wherein each of said different nucleotide sequences consists of 15 to 200 nucleotides.

172. The method of claim 157, wherein each of said different nucleotide sequences consists of 20 to 100 nucleotides.

173. The method of claim 157, wherein each of said different nucleotide sequences consists of 40 to 80 nucleotides.

174. The method of claim 157, wherein each of said different nucleotide sequences consists of 60 nucleotides.

175. The method of claim 157, wherein at least one probe in said plurality of probes contains, in addition to said sequence complementary and hybridizable to a different exon or multiexon, linker sequences.

176. The method of claim 175, wherein said linker sequence comprises a spacer sequence between said sequence complementary and hybridizable to a different exon or multiexon and said support.

177. The method of claim 157, wherein said sequence is complementary to the sequence of a full length exon.

178. The method of claim 157, wherein at least one of said plurality of polynucleotide probes comprises a nucleotide sequence complementary and hybridizable to a multiexon.

179. The method of claim 178, wherein the nucleotide sequence of said at least one polynucleotide probe is complementary to a sequence spanning the splice junction between different exons in said multiexon.

180. The method of claim 178, wherein said sequence is complementary to a sequence comprising a full length exon flanked by sequences from adjacent exon or exons in said multiexon.

181. The method of claim 157, wherein said array of polynucleotide probes further comprises control polynucleotide probes comprising sequences complementary and hybridizable to different introns of said plurality of genes in the genome of said organism.

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182. The method of claim 151 or 157, wherein said expression levels are measured as continuous variables.

183. The method of claim 182, wherein said expression levels are measured as continuous variables and represented as absolute abundance.

184. The method of claim 83 or 151, wherein said cell sample is a human cell sample.

185. The method of claim 83 or 151, wherein said cell sample is a plant cell sample.

186. A method for determining the effect of a perturbation on RNA splicing pathways in a gene, for a plurality of different genes, in a species of an organism, comprising

(a) measuring for a plurality of genes the expression levels of a plurality of individual exons or multiexons in a first cell sample from said species, said first cell sample having been subjected to said perturbation; and

(b) comparing said measured expression levels of said plurality of individual exons or multiexons in said first cell sample to the respective expression levels of said plurality of individual exons or multiexons in a second cell sample from said species, for each of said plurality of genes, said second cell sample not having been subjected to said perturbation, thereby determining the effect of said perturbation on said RNA splicing pathways.

187. The method of claim 186, wherein said plurality of different genes consists of at least 100 different genes.

188. The method of claim 186, wherein said plurality of different genes consists of at least 1,000 different genes.

189. The method of claim 186, wherein said plurality of different genes consists of at least 10,000 different genes.

190. The method of claim 186, wherein in step (a), the expression levels of at least 3 exons in said same gene are measured.

191. The method any one of claims 186-190, further comprising expressing said measured expression level as a ratio of said measured expression level of said plurality of individual exons in said first cell sample to the measured expression level of said plurality of individual exons in said second cell sample.

192. The method of any one of claims 186-190, wherein said measuring is performed by a method comprising

(a) contacting a positionally-addressable array of polynucleotide probes with a sample comprising RNAs or nucleic acids derived therefrom from said cell sample under conditions conducive to hybridization between said probes and said RNAs or nucleic acids, wherein said array comprises a plurality of polynucleotide probes of different nucleotide sequences bound to different

regions of a support, each of said different nucleotide sequences comprising a sequence complementary and hybridizable to a different exon or multiexon of said cell sample; and

(b) measuring hybridization between said probes and said RNAs or nucleic acids.

193. The method of claim 192, further comprising expressing said measured expression level as a ratio of said measured expression level of each of said exons or multiexons in said first cell sample to the measured expression level of corresponding exons or multiexons in said second cell sample.

194. The method of claim 186 further comprising, prior to said comparing step, a step of measuring for said plurality of genes the expression levels of said plurality of individual exons or multiexons in said second cell sample.

195. The method of claim 186 wherein said measured expression levels of said plurality of individual exons or multiexons in said second cell sample is stored in a database on a computer, said database comprising a plurality of measured expression levels of said plurality of individual exons or multiexons in a plurality of cell samples, each cell sample having been subjected to a different perturbation.

196. The method of claim 195 wherein said comparing step is computer-implemented.

197. A computer system for determining the relative level of expression of individual exons in a gene for a plurality of different genes of an organism, said computer system comprising:

one or more processor units; and

one or more memory units connected to said one or more processor units,

said one or more memory units containing one or more programs which cause said one or more processor units to execute steps of:

(a) receiving a data structure of measured expression levels of more than one individual exon or multiexon in each of a plurality of different genes of an organism;

(b) comparing said measured expression level of a first exon or multiexon to the measured expression level of a second exon or multiexon in the same gene, or to the measured expression levels of more than one other exon or

multiexon in said same gene, for each of said plurality of genes to determine differences between said levels; and

(c) displaying said differences;

wherein said differences are a measure of the relative level of expression between individual exons or multiexons in a gene.

198. A computer system for determining alternative splicing between two cell samples of a species of organism, said computer system comprising:

one or more processor units; and

one or more memory units connected to said one or more processor units,

said one or more memory units containing one or more programs which cause said one or more processor units to execute steps of:

(a) receiving a first data structure of measured expression levels of a plurality of individual exons or multiexons in a plurality of genes of a first cell sample of said species of organism and a second data structure of measured expression levels of said plurality of individual exons or multiexons in said plurality of genes of a second cell sample of said species; and

(b) comparing said measured expression levels of said plurality of individual exons or multiexons in said plurality of genes of said first cell sample to said measured expression levels of said plurality of individual exons or multiexons in said plurality of genes of said second cell sample to determine differences between said levels;

wherein the differences in the measured expression levels of said plurality of individual exons or multiexons in said plurality of genes between said first and second cell samples determine alternative splicing between said first and second cell samples.

199. A computer system for determining alternative splicing between two cell samples of a species of organism, said computer system comprising:

one or more processor units; and

one or more memory units connected to said one or more processor units,

said one or more memory units containing one or more programs which cause said one or more processor units to execute steps of:

(a) receiving a first data structure of measured expression levels of a plurality of individual exons or multiexons in a plurality of genes of a first cell sample of said species of organism;

(b) retrieving from a database a second data structure of measured expression

levels of said plurality of individual exons or multiexons in said plurality of genes of a second cell sample of said species; and

(c) comparing said measured expression levels of said plurality of individual exons or multiexons in said plurality of genes of said first cell sample to said measured expression levels of said plurality of individual exons or multiexons in said plurality of genes of said second cell sample to determine differences between said levels;

wherein the differences in the measured expression levels of said plurality of individual exons or multiexons in said plurality of genes between said first and second cell samples determine alternative splicing between said first and second cell samples.

200. The computer system of claim 199, further comprising one or more storage media storing said database.

201. A database contained on a computer readable medium, said database comprising information representing expression levels for a plurality of individual exons or multiexons in each of a plurality of genes in the genome of an organism, wherein said expression levels are each indexed with the identity of said respective individual exon or multiexon.

202. A method for selecting polynucleotide probes for preparation of an array for exon profiling, comprising

(a) selecting a plurality of different nucleotide sequences complementary to each exon or multiexon of a plurality of different exons or multiexons in each of a plurality of different genes in the genome of an organism;

(b) identifying polynucleotide probes in a plurality of polynucleotide probes comprising said selected plurality of different nucleotide sequences, that hybridize to their respective target nucleic acid with a specificity above a threshold specificity level;

(c) ranking the identified polynucleotide probes according to the sensitivity with which each identified polynucleotide probe hybridizes to its respective target nucleic acid; and

(d) selecting one or more different polynucleotide probes from the ranked polynucleotide probes for each exon or multiexon of said plurality of exons or multiexons.

203. The method of claim 202, further comprising synthesizing said selected polynucleotide

probes on the surface of a support, wherein each probe having a distinct sequence is attached to a predefined region on said surface of said support.

204. The method of claim 202, further comprising attaching said selected polynucleotide probes to the surface of a support, wherein each probe having a distinct sequence is attached to a predefined region on said surface of said support.

205. A method for identifying differences in exon or multiexon expression levels that are indicative of alternative splicing among a plurality of samples, comprising comparing the measured expression level of each of a plurality of exons or multiexons in each cell sample of said plurality of cell samples to the measured expression level of the same exon or multiexon in another, different cell sample of said plurality of cell samples to identify differences in the expression levels of one or more exons or multiexons, wherein said identified differences indicate alternative splicings between the two cell samples.

206. The method of claim 205, wherein the expression levels of one or more exons or multiexons in at least one cell sample in said plurality is stored in a database.

207. The method of claim 205 or 206, wherein said plurality of cell samples consists of 10 different cell samples.

208. The method of claim 205 or 206, wherein said plurality of cell samples consists of 25 different cell samples.

209. The method of claim 205 or 206, wherein said plurality of cell samples consists of 50 different cell samples.

210. The method of claim 205 or 206, wherein said plurality of cell samples consists of 100 different cell samples.

211. The method of claim 205 or 206, wherein said plurality of cell samples consists of 1,000 different cell samples.

212. ~~The method of claim 1, 10, 37, 38, 47, 83 or 151, wherein said organism is a fungus.~~

213. The method of claim 86, wherein said organism is a fungus.